IFWO

RAW SEQUENCE LISTING   DATE: 02/10/2004
PATENT APPLICATION: US/10/763,992   TIME: 10:10:47

Input Set : N:\Crf3\RULE60\10763992.RAW.txt
Output Set: N:\CRF4\02102004\J763992.raw

SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 4     (i) APPLICANT: COHEN, Maurice
 5                    FRIEDMAN, Paula N.
 6                    GORDON, Julian
 7                    HODGES, Steven C.
 8                    KLASS, Michael R.
 9                    KRATOCHVIL, Jon D.
10                    ROBERTS-RAPP, Lisa
11                    RUSSELL, John C.
12                    STROUPE, Steven D.
13    (ii) TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
14                             FOR DETECTING DISEASES OF THE PROSTATE
15   (iii) NUMBER OF SEQUENCES: 35
16    (iv) CORRESPONDENCE ADDRESS:
17         (A) ADDRESSEE: Abbott Laboratories
18         (B) STREET: 100 Abbott Park Road
19         (C) CITY: Abbott Park
20         (D) STATE: IL
21         (E) COUNTRY: USA
22         (F) ZIP: 60064-3500
23     (v) COMPUTER READABLE FORM:
24         (A) MEDIUM TYPE: Diskette
25         (B) COMPUTER: IBM Compatible
26         (C) OPERATING SYSTEM: DOS
27         (D) SOFTWARE: FastSEQ for Windows Version 2.0
28    (vi) CURRENT APPLICATION DATA:
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C--> 29   **(A) APPLICATION NUMBER: US/10/763,992**
C--> 30   **(B) FILING DATE: 22-Jan-2004**
```
31         (C) CLASSIFICATION:
35   (vii) PRIOR APPLICATION DATA:
33         (A) APPLICATION NUMBER: US/09/418,887
34         (B) FILING DATE: 15-OCT-1999
36         (A) APPLICATION NUMBER: US/08/946,869
37         (B) FILING DATE: 08-Oct-1997
38  (viii) ATTORNEY/AGENT INFORMATION:
39         (A) NAME: Becker, Cheryl L.
40         (B) REGISTRATION NUMBER: 35,441
41         (C) REFERENCE/DOCKET NUMBER: 5697.US.P1
42    (ix) TELECOMMUNICATION INFORMATION:
43         (A) TELEPHONE: 847/935-1729
44         (B) TELEFAX: 847/938-2623
45         (C) TELEX:
```

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```
46 (2) INFORMATION FOR SEQ ID NO: 1:
47     (i) SEQUENCE CHARACTERISTICS:
48         (A) LENGTH: 367 base pairs
49         (B) TYPE: nucleic acid
50         (C) STRANDEDNESS: single
51         (D) TOPOLOGY: linear
52    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
53         TGCGCNGGAG CCTGAGCGGA GGGTGTGCGC AGCCTCGCCA GCGGGGGCCC CGGGCTGNGC      60
54         CATTGCCTCA CTGAGCCAGC GCCTGCCTNC TACCTCGCCG ACAGCTGGAA CCAGTGCGAC     120
55         CTAGTGGCTC TCACCTGCTT CCTCCTGGGC GTGGGCTGCC GGCTGACCCC GGGTTTGTAC     180
56         CACCTGGGCC GCACTGTCCT CTGCATCGAC TTCATGGTTT TCACGGTGCG GCTGCTTCAC     240
57         ATCTTCACGG TCAACAAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG     300
58         GACGTGTTCT TCTTCCTCTT CTTCCTCGGC GTGTGGCTGG TAGCTATGGG TTGGGCCACG     360
59         GAGGGGT                                                             367
61 (2) INFORMATION FOR SEQ ID NO: 2:
62     (i) SEQUENCE CHARACTERISTICS:
63         (A) LENGTH: 214 base pairs
64         (B) TYPE: nucleic acid
65         (C) STRANDEDNESS: single
66         (D) TOPOLOGY: linear
67    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
68         CAAACAGCTG GGGCCCAAGA TCGTCATCGT GAGCAAGATG ATGAAGGACG TGTTCTTCTT      60
69         CCTCTTCTTC CTCGGCGTGT GGCTGGTAGC CTATGGCGTG GCCACGGAGG GGCTCCTGAG     120
70         GCCACGGGAC AGTGACTTCC CAAGTATCCT GCGCCGCGTC TTCTACCGTC CCTACCTGCA     180
71         GATCTTCGGG CAGATTCCCC AGGAGGACAT GGAC                                214
73 (2) INFORMATION FOR SEQ ID NO: 3:
74     (i) SEQUENCE CHARACTERISTICS:
75         (A) LENGTH: 205 base pairs
76         (B) TYPE: nucleic acid
77         (C) STRANDEDNESS: single
78         (D) TOPOLOGY: linear
79    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
80         CGTGTGGCTG GTAGCCTATG GCGTGGCCAC GGAGGGGCTC CTGAGGCCAC GGGACAGTGA      60
81         CTTCCCAAGT ATCCTGCGCC GCGTCTTCTA CCGTCCCTAC CTGCAGATCT TCGGGCAGAT     120
82         TCCCCAGGAG GACATGGACG TGGCCCTCAT GGAGCACAGC AACTGCTCGT CGGAGCCCGG     180
83         CTTCTGGGCA CACCCTCCTG GGGCC                                          205
85 (2) INFORMATION FOR SEQ ID NO: 4:
86     (i) SEQUENCE CHARACTERISTICS:
87         (A) LENGTH: 256 base pairs
88         (B) TYPE: nucleic acid
89         (C) STRANDEDNESS: single
90         (D) TOPOLOGY: linear
91    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
92         CGGGCAGATT CCCCAGGAGG ACATGGACGT GGCCCTCATG GAGCACAGCA ACTGCTCGTC      60
93         GGAGCCCGGC TTCTGGGCAC ACCCTCCTGG GGCCCAGGCG GGCACCTGCG TCTCCCAGTA     120
94         TGCCAACTGG CTGGTGGTGC TGCTCCTCGT CATCTTCCTG CTCGTGGCCA ACATCCTGCT     180
95         GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTCGGC AAAGTACAGG GCAACAGCGA     240
96         TCTCTACTGG AAGGCG                                                    256
98 (2) INFORMATION FOR SEQ ID NO: 5:
```

```
99        (i) SEQUENCE CHARACTERISTICS:
100           (A) LENGTH: 246 base pairs
101           (B) TYPE: nucleic acid
102           (C) STRANDEDNESS: single
103           (D) TOPOLOGY: linear
104       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
105           GCGATCTCTA CTGGAAGGCG CAGGTTACCG CCTCATCCGG GAATTCCACT CTCGGCCCGC    60
106           GCTGGCCCCG CCCTTTATCG TCATCTCCCA CTTGCGCCTC CTGCTCAGGC AATTGTGCAG   120
107           GCGACCCCGG AGCCCCCAGC CGTCCTCCCC GGCCCTCGAG CATTTCCGGG TTTACCTTTC   180
108           TAAGGAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG CATAAGGAGA ACTTTCTGCT   240
109           GGCACG                                                             246
111  (2) INFORMATION FOR SEQ ID NO: 6:
112        (i) SEQUENCE CHARACTERISTICS:
113           (A) LENGTH: 277 base pairs
114           (B) TYPE: nucleic acid
115           (C) STRANDEDNESS: single
116           (D) TOPOLOGY: linear
117       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
118           GTGCATAAGG AGAACTTTCT GCTGGCACGC GCTAGGGACA AGCGGGAGAG CGACTCCGAG    60
119           CGTCTGAAGC GCACGTCCCA GAAGGTGGAC TTGGCACTGA AACAGCTGGG ACACATCCGC   120
120           GAGTACGAAC AGCGCCTGAA AGTGCTGGAG CGGGAGGTCC AGCAGTGTAG CCGCGTCCTG   180
121           GGGTGGGTGG CCGAGGCCCT GAGCCGCTCT GCCTTGCTGC CCCCAGGTGG GCCGCCACCC   240
122           CCTGACCTGC CTGGGTCCAA AGACTGAGCC CTGCTGG                            277
124  (2) INFORMATION FOR SEQ ID NO: 7:
125        (i) SEQUENCE CHARACTERISTICS:
126           (A) LENGTH: 251 base pairs
127           (B) TYPE: nucleic acid
128           (C) STRANDEDNESS: single
129           (D) TOPOLOGY: linear
130       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
131           GGGTCCAAAG ACTGANCCCT GCTGGCGGAC TTCAAGGAGA AGCCCCCACA GGGGATTTTG    60
132           CTCCTAGAGT AAGGCTCATC TGGGCCTCGG CCCCCGCACC TGGTGGCCTT GTCCTTGAGG   120
133           TGAGCCCCAT GTCCATCTGG GCCACTGTCA GGACCACCTT TGGGAGTGTC ATCCTTACAA   180
134           ACCACAGCAT GCCCGGCTCC TCCCAGAACC AGTCCCAGCC TGGGAGGATC AAGGCCTGGA   240
135           TCCCGGGCCG T                                                       251
137  (2) INFORMATION FOR SEQ ID NO: 8:
138        (i) SEQUENCE CHARACTERISTICS:
139           (A) LENGTH: 223 base pairs
140           (B) TYPE: nucleic acid
141           (C) STRANDEDNESS: single
142           (D) TOPOLOGY: linear
143       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
144           GGCTCATCTG GCCTCGGCC CCCGCACCTG GTGGCCTTGT CCTTGAGGTG AGCCCCATGT    60
145           CCATCTGGGC CACTGTCAGG ACCACCTTTG GGAGTGTCAT CCTTACAAAC CACAGCATGC   120
146           CCGGCTCCTC CCAGAACCAG TCCCAGCCTG GGAGGATCAA GGCCTGGATC CCGGGCCGTT   180
147           ATCCATCTGG AGGCTGCAGG GTCCTTGGGG TAACAGGGAC CAC                     223
149  (2) INFORMATION FOR SEQ ID NO: 9:
150        (i) SEQUENCE CHARACTERISTICS:
151           (A) LENGTH: 2393 base pairs
```

```
152              (B) TYPE: nucleic acid
153              (C) STRANDEDNESS: single
154              (D) TOPOLOGY: linear
155      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
156          AAGGCCACCT CGCCGCTCTC CTGGATGCTG GCCTCGGCAG GCCCCCTGAA CCTGCTTCTT     60
157          TGGGCACTGT TGCTGAAACA GGCACAGATG GCCATGTACT TCTGGGAGAT GGGTTCCAAT    120
158          GCAGTTTCCT CAGCTCTTGG GGCCTGTTTG CTGCTCCGGG TGATGGCACG CCTGGAGCCT    180
159          GACGCTGAGG AGGCAGCACG GAGGAAAGAC CTGGCGTTCA AGTTTGAGGG GATGGGCGTT    240
160          GACCTCTTTG GCGAGTGCTA TCGCAGCAGT GAGGTGAGGG CTGCCCGCCT CCTCCTCCGT    300
161          CGYTGCCCGC TCTGGGGGGA TGCCACTTTG CCTTCCAGGT GGCCATGCAA AGCTGACGSC    360
162          CSTGMCTTCT TTGCCMAGGA TGGGGTACAG TCTCTGCTGA CACAGAAGTG GTGGGGAGAT    420
163          ATGGCCAGCA CTACACCCAT CTGGGCCCTG GTTATCGCGT TCTTTTGCCC TCCACTCATC    480
164          TACACCCGCC TCATCACCTT CAGGAAATCA GAAGAGGAGC CCACACGGGA GGAGCTAGAG    540
165          TTTGACATGG ATAGTGTCAT TAATGGGGAA GGGCCTGTCG GGACGGCGGA CCCAGCCGAG    600
166          AAGACGCCGC TGGGGGTCCC GCGCCAGTCG GGCCGTCCGG GTTGCTGCGG GGGCCGCTGC    660
167          GGGGGGCGCC GGTGCCTACG CCGCTGGTTC CACTTCTGGG GCGCGCCGGT GACCATCTTC    720
168          ATGGGCAACG TGGTCAGCTA CCTGCTGTTC CTGCTGCTTT TCTCGCGGGT GCTGCTCGTG    780
169          GATTTCCAGC CGGCGCCGCC CGGCTCCCTG GAGCTGCTGC TCTATTTCTG GGCTTTCACG    840
170          CTGCTGTGCG AGGAATGCGC CAGGGCCTGA GCGGAGGCGG GGGCAGCCTC GCCAGCGGGG    900
171          GCCCCGGGCC TGGCCATGCC TCACTGAGCC AGCGCCTGCG CCTCTACCTC GCCGACAGCT    960
172          GGAACCAGTG CGACCTAGTG GCTCTCACCT GCTTCCTCCT GGGCGTGGGC TGCCGGCTGA   1020
173          CCCCGGGTTT GTACCACCTG GGCCGCACTG TCCTCTGCAT CGACTTCATG GTTTTCACGG   1080
174          TGCGGCTGCT TCACATCTTC ACGGTCAACA AACAGCTGGG GCCCAAGATC GTCATCGTGA   1140
175          GCAAGATGAT GAAGGACGTG TTCTTCTTCC TCTTCTTCCT CGGCGTGTGG CTGGTAGCCT   1200
176          ATGGCGTGGC CACGGAGGGG CTCCTGAGGC CACGGGACAG TGACTTCCCA AGTATCCTGC   1260
177          GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG GAGGACATGG   1320
178          ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG GCACACCCTC   1380
179          CTGGGGCCCA GGCGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG GTGCTGCTCC   1440
180          TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAA CTTGCTCATT GCCATGTTCA   1500
181          GTTACACATT CGGCAAAGTA CAGGGCAACA GCGATCTCTA CTGGAAGGCG CAGGTTACCG   1560
182          CCTCATCCGG GAATTCCACT CTCGGCCCGC GCTGGCCCCG CCCTTTATCG TCATCTCCCA   1620
183          CTTGCGCCTC CTGCTCAGGC AATTGTGCAG GCGACCCCGG AGCCCCCAGC CGTCCTCCCC   1680
184          GGCCCTCGAG CATTTCCGGG TTTACCTTTC TAAGGAAGCC GAGCGGAAGC TGCTAACGTG   1740
185          GGAATCGGTG CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA   1800
186          CTCCGAGCGT CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA   1860
187          CATCCGCGAG TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG   1920
188          CGTCCTGGGG TGGGTGGCCG AGGCCCTGAG CCGCTCTGCC TTGCTGCCCC CAGGTGGGCC   1980
189          GCCACCCCCT GACCTGCCTG GGTCCAAAGA CTGAGCCCTG CTGGCGGACT TCAAGGAGAA   2040
190          GCCCCCACAG GGGATTTTGC TCCTAGAGTA AGGCTCATCT GGGCCTCGGC CCCCGCACCT   2100
191          GGTGGCCTTG TCCTTGAGGT GAGCCCCATG TCCATCTGGG CCACTGTCAG GACCACCTTT   2160
192          GGGAGTGTCA TCCTTACAAA CCACAGCATG CCCGGCTCCT CCCAGAACCA GTCCCAGCCT   2220
193          GGGAGGATCA AGGCCTGGAT CCCGGGCCGT TATCCATCTG GAGGCTGCAG GGTCCTTGGG   2280
194          GTAACAGGGA CCACAGACCC CTCACCACTC ACAGATTCCT CACACTGGGG AAATAAAGCC   2340
195          ATTTCAGAGG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GGGCGGCCGC GGT          2393
197 (2) INFORMATION FOR SEQ ID NO: 10:
198      (i) SEQUENCE CHARACTERISTICS:
199          (A) LENGTH: 1297 base pairs
200          (B) TYPE: nucleic acid
201          (C) STRANDEDNESS: single
```

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```
202              (D) TOPOLOGY: linear
203        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
204            GAATTCGGCT CGAGCAAACA GCTGGGGCCC AAGATCGTCA TCGTGAGCAA GATGATGAAG     60
205            GACGTGTTCT TCTTCCTCTT CTTCCTCGGC GTGTGGCTGG TAGCCTATGG CGTGGCCACG    120
206            GAGGGGCTCC TGAGGCCACG GGACAGTGAC TTCCCAAGTA TCCTGCGCCG CGTCTTCTAC    180
207            CGTCCCTACC TGCAGATCTT CGGGCAGATT CCCCAGGAGG ACATGGACGT GGCCCTCATG    240
208            GAGCACAGCA ACTGCTCGTC GGAGCCCGGC TTCTGGGCAC ACCCTCCTGG GGCCCAGGCG    300
209            GGCACCTGCG TCTCCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCCTCGT CATCTTCCTG    360
210            CTCGTGGCCA ACATCCTGCT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTCGGC    420
211            AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCCT CATCCGGGAA    480
212            TTCCACTCTC GGCCCGCGCT GGCCCCGCCC TTTATCGTCA TCTCCCACTT GCGCCTCCTG    540
213            CTCAGGCAAT TGTGCAGGCG ACCCCGGAGC CCCCAGCCGT CCTCCCCGGC CCTCGAGCAT    600
214            TTCCGGGTTT ACCTTTCTAA GGAAGCCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT    660
215            AAGGAGAACT TTCTGCTGGC ACGCGCTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG    720
216            AAGCGCACGT CCCAGAAGGT GGACTTGGCA CTGAAACAGC TGGGACACAT CCGCGAGTAC    780
217            GAACAGCGCC TGAAAGTGCT GGAGCGGGAG GTCCAGCAGT GTAGCCGCGT CCTGGGGTGG    840
218            GTGGCCGAGG CCCTGAGCCG CTCTGCCTTG CTGCCCCCAG GTGGGCCGCC ACCCCTGAC     900
219            CTGCCTGGGT CCAAAGACTG AGCCCTGCTG GCGGACTTCA AGGAGAAGCC CCCACAGGGG    960
220            ATTTTGCTCC TAGAGTAAGG CTCATCTGGG CCTCGGCCCC CGCACCTGGT GGCCTTGTCC   1020
221            TTGAGGTGAG CCCCATGTCC ATCTGGGCCA CTGTCAGGAC CACCTTTGGG AGTGTCATCC   1080
222            TTACAAACCA CAGCATGCCC GGCTCCTCCC AGAACCAGTC CCAGCCTGGG AGGATCAAGG   1140
223            CCTGGATCCC GGGCCGTTAT CCATCTGGAG GCTGCAGGGT CCTTGGGGTA ACAGGGACCA   1200
224            CAGACCCCTC ACCACTCACA GATTCCTCAC ACTGGGGAAA TAAAGCCATT TCAGAGGAAA   1260
225            AAAAAAAAAA AAAAAAAAAA AAAAAAGGG CGGCCGC                              1297
227   (2) INFORMATION FOR SEQ ID NO: 11:
228        (i) SEQUENCE CHARACTERISTICS:
229            (A) LENGTH: 68 base pairs
230            (B) TYPE: nucleic acid
231            (C) STRANDEDNESS: single
232            (D) TOPOLOGY: linear
233        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
234            AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC     60
235            CGGGAATT                                                              68
237   (2) INFORMATION FOR SEQ ID NO: 12:
238        (i) SEQUENCE CHARACTERISTICS:
239            (A) LENGTH: 68 base pairs
240            (B) TYPE: nucleic acid
241            (C) STRANDEDNESS: single
242            (D) TOPOLOGY: linear
243        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
244            AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG     60
245            GAATTCCG                                                              68
247   (2) INFORMATION FOR SEQ ID NO: 13:
248        (i) SEQUENCE CHARACTERISTICS:
249            (A) LENGTH: 24 base pairs
250            (B) TYPE: nucleic acid
251            (C) STRANDEDNESS: single
252            (D) TOPOLOGY: linear
253        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/10/2004
PATENT APPLICATION: **US/10/763,992**   TIME: 10:10:48

Input Set : **N:\Crf3\RULE60\10763992.RAW.txt**
Output Set: **N:\CRF4\02102004\J763992.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 53,54,55,56,57,58,59
Seq#:2; Line(s) 68,69,70,71
Seq#:3; Line(s) 80,81,82,83
Seq#:4; Line(s) 92,93,94,95,96
Seq#:5; Line(s) 105,106,107,108,109
Seq#:6; Line(s) 118,119,120,121,122
Seq#:7; Line(s) 131,132,133,134,135
Seq#:8; Line(s) 144,145,146,147
Seq#:9; Line(s) 156,157,158,159,160,161,162,163,164,165,166,167,168,169,170
Seq#:9; Line(s) 171,172,173,174,175,176,177,178,179,180,181,182,183,184,185
Seq#:9; Line(s) 186,187,188,189,190,191,192,193,194,195
Seq#:10; Line(s) 204,205,206,207,208,209,210,211,212,213,214,215,216,217
Seq#:10; Line(s) 218,219,220,221,222,223,224,225
Seq#:11; Line(s) 234,235
Seq#:12; Line(s) 244,245
Seq#:13; Line(s) 254
Seq#:14; Line(s) 263
Seq#:15; Line(s) 272
Seq#:16; Line(s) 281
Seq#:17; Line(s) 290
Seq#:18; Line(s) 299
Seq#:19; Line(s) 308
Seq#:20; Line(s) 317
Seq#:21; Line(s) 326
Seq#:22; Line(s) 335
Seq#:23; Line(s) 344
Seq#:24; Line(s) 353

VERIFICATION SUMMARY   DATE: 02/10/2004
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Output Set: **N:\CRF4\02102004\J763992.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:361 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:454 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26
L:466 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28
L:488 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:499 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=31
L:521 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:532 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=33